



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/674,379

Source: PGT/09

Date Processed by STIC: 4/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/674,379

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,379

DATE: 04/25/2001
TIME: 07:41:15

Input Set : A:\es.txt
Output Set: N:\CRF3\04252001\I674379.raw

Does Not Comply
Corrected Diskette Needed
see pp. 4, 6

3 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
5 <120> TITLE OF INVENTION: A novel polypeptide, a cDNA encoding the polypeptide
6 and utilization thereof
8 <130> FILE REFERENCE: Q61531
SV-> 10 <140> CURRENT APPLICATION NUMBER: US/09/674,379
C-> 11 <141> CURRENT FILING DATE: 2000-10-30
13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02284
14 <151> PRIOR FILING DATE: 1999-04-28
16 <150> PRIOR APPLICATION NUMBER: JP HEI 10-119731
17 <151> PRIOR FILING DATE: 1998-04-28
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1344
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <400> SEQUENCE: 1
29 atgccaggat taaaaaggat actcactgtt accatcttgg cactctggct tccacatcct 60
30 gggatgcac agcagcagtg cacaacggc tttgacctgg accggccagtc aggacagtgt 120
31 ctagatattg atgaatcccg gaccatccct gaggcttgcgt gtggggacat gatgtgtgtc 180
32 aaccagaatg gcgggtattt gtgcattccct cgaaccaacc cagtgtatcg agggcattac 240
33 tcaaattccct actctacatc ctactcaggc ccatacccaag cagcggccccc accagttacca 300
34 gcttccaact accccacgtt ttcaggccct cttgtctgcc gctttgggtt tcagatggat 360
35 gaaggcaacc agtgtgtgga tgtggacgag tgtcaacag actcacacca gtgcaaccct 420
36 acccagatct gtatcaacac tgaaggaggt tacacctgtt cctgcaccga tgggtactgg 480
37 cttctggaaag ggcagtcgtt agatattgtt gaatgtcgat atggttactg ccagcagctc 540
38 tgtgcaatg ttccaggatc ctattcctgt acatgcaacc ctgggttccac cctcaacgac 600
39 gatggaaagg tttgccaaga tgtgaacgag tgcgaaactg agaattccctg tggtagacc 660
40 tgtgtcaaca cctatggctc tttcatctgc cgctgtgacc caggatatga acttgaggaa 720
41 gatggcatcc actgcagtga tatggacgag tgcagttctt ccgagttccct ctgtcaacac 780
42 gatgtgtga accagccggg ctcatacttc tgctctgcc ctccaggctt cgtcctgtt 840
43 gatgataacc gaagctgcac gatatcaat gaatgtgagc accgaaacca cacgtgtacc 900
44 tcactgcaga cttgtacaa tctacaaggg ggcttcaat gtattgtatcc catcagctgt 960
45 gaggagcctt atctgtgtat tggtaaaac cgctgtatgt gtcctgtga gcacaccaggc 1020
46 tgcagagacc agccattcac catcctgtat cgggacatgg atgtgggtgc aggacgctcc 1080
47 ttcctgtgtc acatctcca gatgcaagca acaaccggat accctgtgc ctattacatt 1140
48 ttccagatca aatctggcaa cgagggtcga gagttctata tgcggcaaac agggcctatc 1200
49 agtgccaccc tggtgatgac acgccccatc aaaggccctc gggacatcca gctggacttg 1260
50 gagatgatca ctgtcaacac tgcattcaac ttcagaggca gtcctgtat ccgactgcgg 1320
51 atatatgtgtc cgccgtatcc gttc 1344
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 2233
56 <212> TYPE: DNA
57 <213> ORGANISM: Mus musculus
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse
61 embryonic heart

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Input Set : A:\es.txt
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63 <220> FEATURE:
64 <221> NAME/KEY: CDS
65 <222> LOCATION: (75)..(1418)
67 <220> FEATURE:
68 <221> NAME/KEY: sig_peptide
69 <222> LOCATION: (75)..(143)
71 <220> FEATURE:
72 <221> NAME/KEY: mat_peptide
73 <222> LOCATION: (144)..(1418)
75 <400> SEQUENCE: 2
76 aattcggcac gagcccccagt cccaccgcag agcctgcctt cctcgcgtcg cttctccctcc 60
78 cgcgcatctt ggat atg cca gga tta aaa agg ata ctc act gtt acc atc 110
79 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
80 -20 -15
82 ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag tgc aca 158
83 Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
84 -10 -5 -1 1 5
86 aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
87 Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
88 10 15 20
90 gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254
91 Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
92 25 30 35
94 aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
95 Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
96 40 45 50
98 cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350
99 Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
100 55 60 65
102 cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398
103 Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
104 70 75 80 85
106 agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag 446
107 Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln
108 90 95 100
110 tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct 494
111 Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro
112 105 110 115
114 acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc 542
115 Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr
116 120 125 130
118 gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt 590
119 Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys
120 135 140 145
122 cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat 638
123 Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr
124 150 155 160 165
126 tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct 686
127 Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser

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PATENT APPLICATION: US/09/674,379

DATE: 04/25/2001
TIME: 07:41:15

Input Set : A:\es.txt
Output Set: N:\CRF3\04252001\I674379.raw

128	170	175	180	
130	tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc			734
131	Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr			
132	185	190	195	
134	tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat			782
135	Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr			
136	200	205	210	
138	gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc			830
139	Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser			
140	215	220	225	
142	ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca			878
143	Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser			
144	230	235	240	245
146	tac ttc tgc tcg tgc cct cca ggc tac gtc ctg ttg gat gat aac cga			926
147	Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg			
148	250	255	260	
150	agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc			974
151	Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr			
152	265	270	275	
154	tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat			1022
155	Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Phe Lys Cys Ile Asp			
156	280	285	290	
158	ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt			1070
159	Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys			
160	295	300	305	
162	atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc			1118
163	Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile			
164	310	315	320	325
166	ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac			1166
167	Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp			
168	330	335	340	
170	atc ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att			1214
171	Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile			
172	345	350	355	
174	ttc cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa			1262
175	Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln			
176	360	365	370	
178	aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg			1310
179	Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly			
180	375	380	385	
182	cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc			1358
183	Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val			
184	390	395	400	405
186	atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tcg			1406
187	Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser			
188	410	415	420	
190	cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag			1458
191	Gln Tyr Pro Phe			
192	425			

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Input Set : A:\es.txt
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194 caccgaggga cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac 1518
 196 ctttctgtc gaatatctcc tggggcatc agcctagcat cttgaccat atctgtacta 1578
 198 ttgcagatgg tcactctgaa ggacaccctg ccctcagttc ctatgtatca gttatccaaa 1638
 200 agtggtcattt ttagccctg atatgagggtt gccagtgact cttcaaaagcc ttccatttat 1698
 202 ttccatcggtt ttataaaaaa gaaaatagat tagatttgct ggggtatgag tcctcgaaagg 1758
 204 ttcaaaagac tgagtggctt gctctcacct cttcctctcc ttccctccatc tcttgcgtca 1818
 206 ttgcgtctt gcaaaaagtc tcatgggctc gtggaaatg ctggaaatag ctatgttgc 1878
 208 tcttgcgtgt tctgagaagg ctatgggaac acaccacagc aggatcgaag gttttatag 1938
 210 agtctatccc aaaatcacat ctgttatttt cagcataaaa gaaattttag ttgtctttaa 1998
 212 aatttgcgtatg agtggtaac ctttcttata tcattttgag gcttcttaaa gtggtagaat 2058
 214 tcctccaaa ggcctcagat acatgttata ttcagtcctt ccaacctcat ctttcctgc 2118
 W--> 216 atcttagccc agttttacg aagaccctt aatcatgctt ~~tttaagat~~ ttttacccaa 2178
 218 ctgcgttggaa agacagaggt atccagactg attaataat tgaagaaaaaaa 2233
 221 <210> SEQ ID NO: 3
 222 <211> LENGTH: 448
 223 <212> TYPE: PRT
 224 <213> ORGANISM: Mus musculus *(2207) never identified whenever (2217, 2227 or 2237 is shown)*
 225 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse
 228 <400> SEQUENCE: 3
 229 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Trp
 230 -20 -15 -10
 232 Leu Pro His Pro Gly Asn Ala Gln Gln Cys Thr Asn Gly Phe Asp
 233 -5 -1 1 5
 235 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
 236 10 15 20 25
 238 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
 239 30 35 40
 241 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
 242 45 50 55
 244 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
 245 60 65 70
 247 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val
 248 75 80 85
 250 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val
 251 90 95 100 105
 253 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
 254 110 115 120
 256 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
 257 125 130 135
 259 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
 260 140 145 150
 262 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
 263 155 160 165
 265 Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val
 266 170 175 180 185
 268 Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
 269 190 195 200
 271 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
 272 205 210 215

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Input Set : A:\es.txt
Output Set: N:\CRF3\04252001\I674379.raw

274 Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
275 220 225 230
277 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser
278 235 240 245
280 Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
281 250 255 260 265
283 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr
284 270 275 280
286 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys
287 285 290 295
289 Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala
290 300 305 310
292 Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
293 315 320 325
295 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
296 330 335 340 345
298 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
299 350 355 360
301 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
302 365 370 375
304 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
305 380 385 390
307 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
308 395 400 405
310 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
311 410 415 420 425
315 <210> SEQ ID NO: 4
316 <211> LENGTH: 423
317 <212> TYPE: PRT
318 <213> ORGANISM: Mus musculus
320 <400> SEQUENCE: 4
321 Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
322 1 5 10 15
324 Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
325 20 25 30
327 Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
328 35 40 45
330 Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
331 50 55 60
333 Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
334 65 70 75 80
336 Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
337 85 90 95
339 Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
340 100 105 110
342 Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
343 115 120 125
345 Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
346 130 135 140

<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

cgattgaatt ctagaccctgc ctgcgagⁿⁿⁿⁿ nnnnn

see
item 10 on

35

Error
summary sheet

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/674,379

DATE: 04/25/2001
TIME: 07:41:16

Input Set : A:\es.txt
Output Set: N:\CRF3\04252001\I674379.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1277 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:1277 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:1277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16